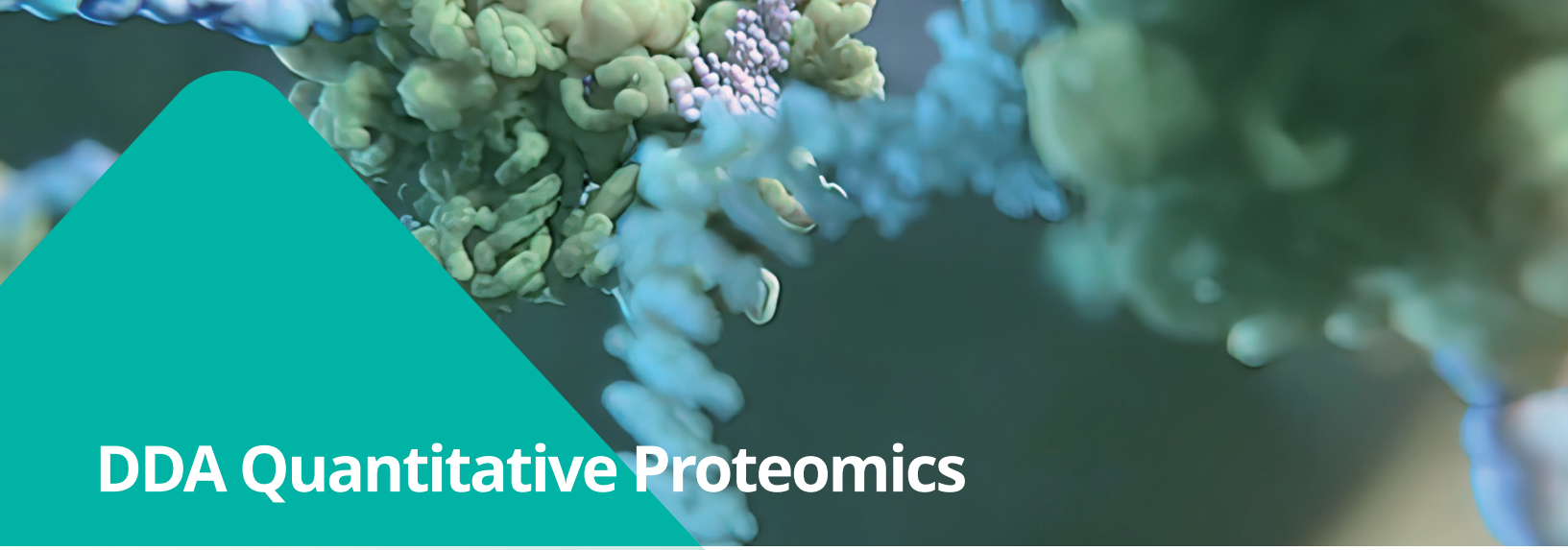


DDA Quantitative Proteomics

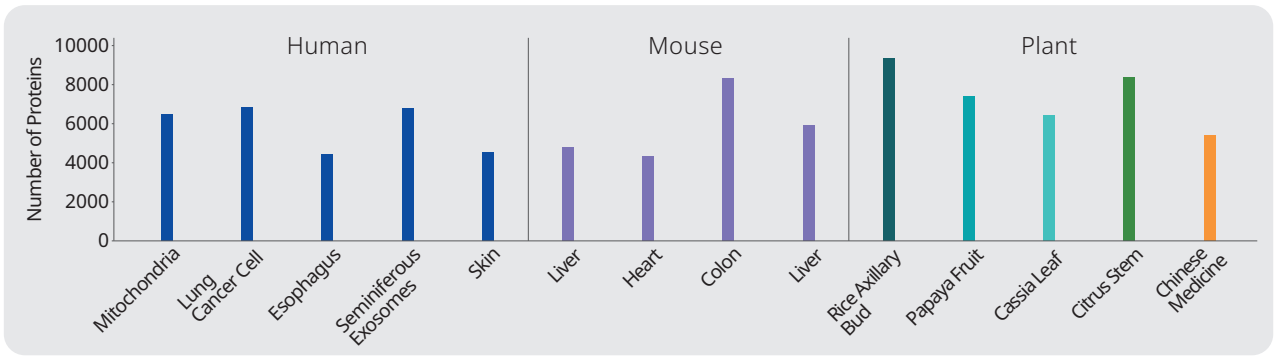
DDA Quantitative Proteomics utilizes timsTOF HT spectrometer and the ddaPASEF (parallel accumulation-serial fragmentation) acquisition mode to achieve qualitative and quantitative analysis. DDA Quantitative Proteomics offers simplicity in operation, free from expensive labeling reagents, reduced data complexity, and improved detection sensitivity.

- Sample specific protein extraction
- Minimize sample manipulation for intact biological characteristics
- Accurate qualitative and quantitative analysis with excellent data stability
- High sensitivity with more low-abundance proteins detection

Data-Dependent Acquisition Mode

In the ddaPASEF acquisition mode, precursor ions with high ion intensity are selected from the MS1 spectra to set the mass spectrum scan range to specific narrow mass windows. The selected target precursor ions are sequentially fragmented in the MS2 spectra, with their retention time, mass-to-charge ratio, ion intensity, and ion mobility recorded for subsequent protein qualitative and quantitative analysis.

Project Experience



Average number of proteins identified

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